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1647

1600

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p.6

RAW SEQUENCE LISTING   DATE: 11/04/2002
PATENT APPLICATION: US/09/830,972   TIME: 13:39:14

Input Set : A:\10200-003.txt
Output Set: N:\CRF4\11042002\I830972.raw

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 4 <110> APPLICANT: Schwab, M.
 5        Chen, M.
 7 <120> TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO
 8        GENES AND METHODS BASED THEREON
11 <130> FILE REFERENCE: 10200-003-999
13 <140> CURRENT APPLICATION NUMBER: 09/830,972
14 <141> CURRENT FILING DATE: 2001-09-24
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/26160
17 <151> PRIOR.FILING DATE: 1999-11-05
19 <150> PRIOR APPLICATION NUMBER: 60/107,446
20 <151> PRIOR FILING DATE: 1998-11-06
22 <160> NUMBER OF SEQ ID NOS: 51
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 3741
28 <212> TYPE: DNA
29 <213> ORGANISM: Rattus sp.
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (253)...(3741)
35 <400> SEQUENCE: 1
36  attgctcgtc tgggcggcgg cggcggctgc agcctgggac agggcgggtg gcacatctcg      60
37  atcgcgaagg cagcagaagc agtctcattg ttccgggagc cgtcgcctct gcaggttctt     120
38  cggctcggct cggcacgact cggcctgcct ggccctgcc agtcttgccc aaccccaca      180
39  accgcccgcg actctgagga gaagcggccc tgcggcggct gtagctgcag catcgtcggc     240
40  gacccgccag cc atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc     291
41                Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser
42                 1               5                  10
44  acg gac agc ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg     339
45  Thr Asp Ser Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val
46       15                  20                  25
48  acg gag ccc gag gac gag gag gac gag gag gag gag gag gac gag gag     387
49  Thr Glu Pro Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu
50   30                  35                  40                  45
52  gag gac gac gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc     435
53  Glu Asp Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro
54                   50                  55                  60
56  gca gcc ggg ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg     483
57  Ala Ala Gly Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro
58                   65                  70                  75
59  ctg ctg gac ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg     531
60  Leu Leu Asp Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro
61                   80                  85                  90
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63   ctg ccg gcc gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa     579
64   Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu
65        95              100             105
67   cgc agc ccc gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc     627
68   Arg Ser Pro Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val
69   110             115             120             125
71   ctg ccc tcc aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg     675
72   Leu Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
73               130             135             140
75   cct ccg ccg cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc     723
76   Pro Pro Pro Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro
77               145             150             155
79   cct tcc acg ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat     771
80   Pro Ser Thr Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp
81           160             165             170
83   gag acc ctt ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc     819
84   Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser
85       175             180             185
87   tct gca gaa aaa att atg gat ttg atg gag cag cca ggt aac act gtt     867
88   Ser Ala Glu Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val
89   190             195             200             205
91   tcg tct ggt caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc     915
92   Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala
93               210             215             220
95   tct ctt cct tct cta tct cct ctc tca act gtt tct ttt aaa gaa cat     963
96   Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His
97               225             230             235
99   gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca att     1011
100  Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile
101          240             245             250
103  gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg gca aca     1059
104  Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr
105      255             260             265
107  aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat     1107
108  Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr
109  270             275             280             285
111  tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc     1155
112  Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala
113              290             295             300
114  ata tta gta gaa aac act aag gaa gaa gta att gtg agg agt aaa gac     1203
115  Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp
116              305             310             315
118  aaa gag gat tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca     1251
119  Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser
120          320             325             330
122  cct gtg ggt aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac     1299
123  Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp
124          335             340             345
126  att ttt aat gaa atg cag atg tca gta gta gca cct gtg agg gaa gag     1347
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127  Ile Phe Asn Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu
128  350             355             360             365
130  tat gca gac ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act    1395
131  Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr
132              370             375             380
134  tat gag gga agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt    1443
135  Tyr Glu Gly Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser
136              385             390             395
138  aaa gtg gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt    1491
139  Lys Val Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu
140              400             405             410
142  ggg aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc    1539
143  Gly Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
144          415             420             425
146  cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc    1587
147  Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser
148  430             435             440             445
150  ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct ttg tta    1635
151  Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu
152              450             455             460
154  gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa    1683
155  Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu
156              465             470             475
158  agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca aat    1731
159  Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn
160          480             485             490
162  cct ttc ctt gta gca gta cag gat tct gag gca gat tat gtt aca aca    1779
163  Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr
164          495             500             505
166  gat acc tta tca aag gtg act gag gca gca gtg tca aac atg cct gaa    1827
167  Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu
168  510             515             520             525
169  ggt ctg acg cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat    1875
170  Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn
171              530             535             540
173  gaa gcc aca ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc    1923
174  Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val
175              545             550             555
177  caa aca tca gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt    1971
178  Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu
179              560             565             570
181  tgc cca tca ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct    2019
182  Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro
183          575             580             585
185  gat att gtt atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt    2067
186  Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly
187  590             595             600             605
189  gct tct gta gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca    2115
190  Ala Ser Val Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro
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191                 610                 615                 620
193   gtt agt tat gac agt ata aag ctt gag cct gaa aac ccc cca cca tat       2163
194   Val Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr
195                 625                 630                 635
197   gaa gaa gcc atg aat gta gca cta aaa gct ttg gga aca aag gaa gga       2211
198   Glu Glu Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly
199                 640                 645                 650
201   ata aaa gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct       2259
202   Ile Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
203         655                 660                 665
205   cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc       2307
206   Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser
207   670                 675                 680                 685
209   act gag cca agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc       2355
210   Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe
211                 690                 695                 700
213   gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct       2403
214   Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro
215                 705                 710                 715
217   gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc       2451
218   Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val
219                 720                 725                 730
221   cca caa aca caa gag gag gct gtg atg ctc atg aag gag agt ctc act       2499
222   Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr
223         735                 740                 745
225   gaa gtg tct gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc       2547
226   Glu Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala
227   750                 755                 760                 765
229   tca cct cag gag cta gga aag cca tat tta gag tct ttt cag ccc aat       2595
230   Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn
231                 770                 775                 780
233   tta cat agt aca aaa gat gct gca tct aat gac att cca aca ttg acc       2643
234   Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr
235                 785                 790                 795
237   aaa aag gag aaa att tct ttg caa atg gaa gag ttt aat act gca att       2691
238   Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile
239                 800                 805                 810
241   tat tca aat gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa       2739
242   Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu
243         815                 820                 825
245   agt gaa aca ttt tca gat tca tct ccg att gag ata ata gat gaa ttt       2787
246   Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe
247   830                 835                 840                 845
249   ccc acg ttt gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag       2835
250   Pro Thr Phe Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu
251                 850                 855                 860
253   tac act gat cta gaa gta tcc gac aaa agt gaa att gct aat atc caa       2883
254   Tyr Thr Asp Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln
255                 865                 870                 875
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```
257  agc ggg gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct   2931
258  Ser Gly Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser
259          880               885               890
261  ttc aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc   2979
262  Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
263          895               900               905
265  tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca aat   3027
266  Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn
267  910               915               920               925
269  gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc   3075
270  Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser
271              930               935               940
273  aaa tca ctt acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag   3123
274  Lys Ser Leu Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu
275              945               950               955
277  aaa gag gac aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa   3171
278  Lys Glu Asp Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys
279              960               965               970
281  act tca gtt gtt gac ctc ctc tac tgg aga gac att aag aag act gga   3219
282  Thr Ser Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly
283              975               980               985
285  gtg gtg ttt ggt gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc   3267
286  Val Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe
287  990               995               1000              1005
289  agc att gtc agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg   3315
290  Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val
291              1010              1015              1020
293  act atc agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa   3363
294  Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys
295              1025              1030              1035
297  tca gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct   3411
298  Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
299              1040              1045              1050
301  ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt cat   3459
302  Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
303          1055              1060              1065
305  gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt gat gat   3507
306  Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp
307  1070              1075              1080              1085
309  tta gtt gat tcc ctg aag ttt gca gtg ttg atg tgg gtg ttt act tat   3555
310  Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr
311              1090              1095              1100
313  gtt ggt gcc ttg ttc aat ggt ctg aca cta ctg att tta gct ctg atc   3603
314  Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile
315              1105              1110              1115
317  tca ctc ttc agt att cct gtt att tat gaa cgg cat cag gtg cag ata   3651
318  Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile
319          1120              1125              1130
321  gat cat tat cta gga ctt gca aac aag agt gtt aag gat gcc atg gcc   3699
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/04/2002
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 2
Seq#:6; Xaa Pos. 2,5
Seq#:29; Xaa Pos. 187,188,189,190,221,328,477
Seq#:30; Xaa Pos. 469
Seq#:35; N Pos. 110
Seq#:36; N Pos. 91
Seq#:37; N Pos. 170,275
Seq#:38; N Pos. 371,444,474,501,506,524,544,561,580,614,620
Seq#:39; N Pos. 149,198,207,246,312,317
Seq#:42; N Pos. 383,402,421,433,441
Seq#:47; N Pos. 3,6,12,15,18
Seq#:48; N Pos. 3,6,9,12,15
Seq#:49; N Pos. 3,6,12,15,20
Seq#:50; N Pos. 3,6,9,12,15,18,21
Seq#:51; N Pos. 9,12,24